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(54) Title: METHODS FOR MAKING POLYKETIDES					
<p>(57) Abstract</p> <p>The stereochemical centers of a polyketide can be changed by replacement of ketosynthase domains in the polyketide synthase (PKS) enzyme that produces the polyketide. The specificity of the AT domains of a PKS is determined by a hypervariable region that can be replaced or altered to change the specificity of the AT domain from a naturally occurring extender unit to another naturally or non-naturally occurring extender unit. Non-naturally occurring extender units, including methylmalonyl N-acetyl cysteamine thioester can be incorporated into polyketides in recombinant host cells or in cell-free systems to make polyketides.</p>					

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METHODS FOR MAKING POLYKETIDES

Cross-Reference to Related Applications

5 This application claims priority to Serial Nos. 60/091,526 and 60/091,610, both filed 2 July 1998, and both of which are incorporated herein by reference in their entirety.

Reference to Government Funding

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Field of the Invention

The present invention relates to polyketides and the polyketide synthase (PKS) enzymes that produce them. The invention also relates generally to genes encoding PKS enzymes and to recombinant host cells containing such genes and in which expression of such genes leads to the production of polyketides. Thus, the invention relates to the fields of chemistry, molecular biology, and agricultural, medical, and veterinary technology.

20 Background of the Invention

Polyketides are a class of compounds synthesized from 2-carbon units through a series of condensations and subsequent modifications. Polyketides occur in many types of organisms, including fungi and mycelial bacteria, in particular, the actinomycetes. Polyketides are biologically active molecules with a wide variety of structures, and the 25 class encompasses numerous compounds with diverse activities. Tetracycline, erythromycin, epothilone, FK-506, FK-520, narbomycin, picromycin, rapamycin, spinocyn, and tylosin are examples of polyketides. Given the difficulty in producing polyketide compounds by traditional chemical methodology, and the typically low production of polyketides in wild-type cells, there has been considerable interest in 30 finding improved or alternate means to produce polyketide compounds.

The biosynthetic diversity of polyketides is generated by repetitive condensations of simple monomers by PKSs that mimic fatty acid synthases but are capable of additional processing reactions (see Carreras *et al.*, 1997, *Topic in Current Chemistry*,

Springer-Verlag, Berlin; and Staunton *et al.*, 1997, *Chem. Rev.* 97: 2611-2629, each of which is incorporated herein by reference). For instance, the deoxyerythronolide-B (DEBS-B) synthase catalyzes the chain extension of a primer with several methylmalonyl coenzyme A (MeMalCoA) extender units to produce the erythromycin core (see Khosla, 5 1997, *Chem. Rev.* 97: 2577-2590, and Hopwood, 1997, *Chem. Rev.* 97: 2465-2495, each of which is incorporated herein by reference).

The cloning, analysis, and recombinant DNA technology of genes that encode PKS enzymes allows one to manipulate a known PKS gene cluster either to produce the polyketide synthesized by that PKS at higher levels than occur in nature or in hosts that 10 otherwise do not produce the polyketide. The technology also allows one to produce molecules that are structurally related to, but distinct from, the polyketides produced from known PKS gene clusters. See, e.g., PCT publication Nos. WO 93/13663; 95/08548; 96/40968; 97/02358; 98/27203; and 98/49315; United States Patent Nos. 4,874,748; 5,063,155; 5,098,837; 5,149,639; 5,672,491; 5,712,146; 5,830,750; and 5,843,718; and 15 Fu *et al.*, 1994, *Biochemistry* 33: 9321-9326; McDaniel *et al.*, 1993, *Science* 262: 1546-1550; and Rohr, 1995, *Angew. Chem. Int. Ed. Engl.* 34(8): 881-888, each of which is incorporated herein by reference.

PKSs catalyze the biosynthesis of polyketides through repeated, decarboxylative Claisen condensations between acylthioester building blocks. The building blocks used 20 to form complex polyketides are typically acylthioesters, such as acetyl, butyryl, propionyl, malonyl, hydroxymalonyl, methylmalonyl, and ethylmalonyl CoA. Two major types of PKS enzymes are known; these differ in their composition and mode of synthesis of the polyketide synthesized. These two major types of PKS enzymes are commonly referred to as Type I or "modular" and Type II "iterative" PKS enzymes.

25 In the Type I or modular PKS enzyme group, a set of separate catalytic active sites (each active site is termed a "domain", and a set thereof is termed a "module") exists for each cycle of carbon chain elongation and modification in the polyketide synthesis pathway. The typical modular PKS is composed of several large polypeptides, which can be segregated from amino to carboxy terminii into a loading module, multiple extender 30 modules, and a releasing (or thioesterase) domain. The PKS enzyme known as 6-deoxyerythronolide B synthase (DEBS) is a typical Type I PKS. In DEBS, there is a loading module, six extender modules, and a thioesterase (TE) domain. The loading module, six extender modules, and TE of DEBS are present on three separate proteins

(designated DEBS-1, DEBS-2, and DEBS-3, with two extender modules per protein). Each of the DEBS polypeptides is encoded by a separate open reading frame (ORF) or gene; these genes are known as *eryA1*, *eryAII*, and *eryAIII*. See Caffrey *et al.*, 1992, *FEBS Letters* 304: 205, and U.S. Patent No. 5,824,513, each of which is incorporated herein by reference. (See Figure 2.) There is considerable interest in the genetic and chemical reprogramming of modular PKSs (see, e.g., Khosla, 1997, *Chem. Rev.* 97: 2577-2590, and Staunton *et al.*, 1997, *Chem. Rev.* 97: 2611-2629, each of which is incorporated herein by reference).

Generally, the loading module is responsible for binding the first building block used to synthesize the polyketide and transferring it to the first extender module. The loading module of DEBS consists of an acyltransferase (AT) domain and an acyl carrier protein (ACP) domain. Another type of loading module utilizes an inactivated KS, an AT, and an ACP. This inactivated KS is in some instances called KS^Q, where the superscript letter is the abbreviation for the amino acid, glutamine, that is present instead of the active site cysteine required for ketosynthase activity. In other PKS enzymes, including the FK-520 PKS, the loading module incorporates an unusual starter unit and is composed of a CoA ligase activity domain. In any event, the loading module recognizes a particular acyl-CoA (usually acetyl or propionyl but sometimes butyryl) and transfers it as a thiol ester to the ACP of the loading module.

The AT on each of the extender modules recognizes a particular extender-CoA (malonyl or alpha-substituted malonyl, i.e., methylmalonyl, ethylmalonyl, and carboxylglycolyl) and transfers it to the ACP of that extender module to form a thioester. Each extender module is responsible for accepting a compound from a prior module, binding a building block, attaching the building block to the compound from the prior module, optionally performing one or more additional functions, and transferring the resulting compound to the next module.

Each extender module of a modular PKS contains a ketosynthase (KS), AT, ACP, and zero, one, two, or three enzymes that modify the beta-carbon of the growing polyketide chain. A typical (non-loading) minimal Type I PKS extender module is exemplified by extender module three of DEBS, which contains a KS domain, an AT domain, and an ACP domain. These three domains are sufficient to activate a 2-carbon extender unit and attach it to the growing polyketide molecule. The next extender

module, in turn, is responsible for attaching the next building block and transferring the growing compound to the next extender module until synthesis is complete.

Once the PKS is primed with acyl- and malonyl-ACPs, the acyl group of the loading module migrates to form a thiol ester (trans-esterification) at the KS of the first 5 extender module; at this stage, extender module one possesses an acyl-KS adjacent to a malonyl (or substituted malonyl) ACP. The acyl group derived from the loading module is then covalently attached to the alpha-carbon of the malonyl group to form a carbon-carbon bond, driven by concomitant decarboxylation, and generating a new acyl-ACP that has a backbone two carbons longer than the loading building block (elongation or 10 extension).

The polyketide chain, growing by two carbons each extender module, is sequentially passed as covalently bound thiol esters from extender module to extender module, in an assembly line-like process. The carbon chain produced by this process alone would possess a ketone at every other carbon atom, producing a polyketone, from 15 which the name polyketide arises. Most commonly, however, additional enzymatic activities modify the beta keto group of each two carbon unit just after it has been added to the growing polyketide chain but before it is transferred to the next module.

Thus, in addition to the minimal module containing KS, AT, and ACP domains necessary to form the carbon-carbon bond and as noted above, modules may contain a 20 ketoreductase (KR) domain that reduces the keto group to an alcohol. Modules may also contain a KR domain plus a dehydratase (DH) domain that dehydrates the alcohol to a double bond. Modules may also contain a KR domain, a DH domain, and an enoylreductase (ER) domain that converts the double bond product to a saturated single bond using the beta carbon as a methylene function. An extender module can also 25 contain other enzymatic activities, such as, for example, a methylase or dimethylase activity.

After traversing the final extender module, the polyketide encounters a releasing domain that cleaves the polyketide from the PKS and typically cyclizes the polyketide. For example, final synthesis of 6-dEB is regulated by a TE domain located at the end of 30 extender module six. In the synthesis of 6-dEB, the TE domain catalyzes cyclization of the macrolide ring by formation of an ester linkage. In FK-506, FK-520, rapamycin, and similar polyketides, the ester linkage formed by the TE activity is replaced by a linkage formed by incorporation of a pipecolate acid residue. The enzymatic activity that

catalyzes this incorporation for the rapamycin enzyme is known as RapP, encoded by the *rapP* gene. The polyketide can be modified further by tailoring enzymes; these enzymes add carbohydrate groups or methyl groups, or make other modifications, i.e., oxidation or reduction, on the polyketide core molecule. For example, 6-dEB is hydroxylated at C6 5 and C12 and glycosylated at C3 and C5 in the synthesis of erythromycin A.

In PKS polypeptides, the regions that encode enzymatic activities (domains) are separated by linker or "scaffold"-encoding regions. These scaffold regions encode amino acid sequences that space the domains at the appropriate distances and in the correct order. Thus, the linker regions of a PKS protein collectively can be considered to encode 10 a scaffold into which the various domains (and thus modules) are placed in a particular order and spatial arrangement. Generally, this organization permits PKS domains of different or identical substrate specificities to be substituted (usually at the DNA level) between PKS enzymes by various available methodologies. Thus, there is considerable 15 flexibility in the design of new PKS enzymes with the result that known polyketides can be produced more effectively, and novel polyketides useful as pharmaceuticals or for other purposes can be made.

There remains a need for new methods and reagents for making polyketides. In particular, methods for altering the stereochemistry of polyketides by altering the PKS enzymes that produce the polyketides, as well as methods for altering the specificity of 20 AT domains of PKS enzymes, without substantial loss of PKS activity are needed. The present invention helps meet the need for such nucleic acid compounds by providing new methods and reagents for manipulating PKS genes.

Disclosure of the Invention

25 In one embodiment, the invention provides a method for altering the specificity of an acyltransferase (AT) domain of a polyketide synthase, which method comprises the step of altering the amino acid sequence of the hypervariable region of the AT domain without changing at least a portion of the remaining AT domain amino acid sequence. In one embodiment, the specificity of the AT domain is changed from one naturally occurring starter or extender unit to another. The correct specificity may, if desired, be 30 assured by altering the hypervariable region to mimic that of an AT of the desired specificity such as those shown in Figure 1.

In another embodiment, the invention provides a method for changing the specificity of an AT domain of a PKS including changing it from that for the naturally occurring starter or extender unit to a starter or extender unit that is not naturally incorporated, said method comprising the steps of altering the amino acid sequence of the 5 hypervariable region of the AT domain by mutagenesis, and if necessary, assessing the resulting specificity by contacting the PKS comprising the altered AT domain with one or more starter or extender units that are not incorporated into polyketides in nature, and identifying whether the altered AT domain can incorporate the tested starter or extender unit. In related embodiments, the invention provides novel PKS enzymes capable of 10 incorporating starter or extender units not natively incorporated and novel polyketides produced thereby.

In another embodiment, the present invention provides non-native extender substrates for PKS enzymes and methods of making such extender substrates. In one embodiment, these non-native extender substrates are used to make polyketides in a cell-free system and in host cells that do not naturally produce polyketides but which can 15 produce polyketides when provided with a recombinant PKS and the appropriate substrates.

In another embodiment, the invention provides a method for altering the stereochemistry of a polyketide by replacing a KS domain in the PKS that produces the 20 polyketide with a KS domain that provides the desired stereochemistry.

These and other embodiments, modes, and aspects of the invention are described in more detail in the following description, the examples, and claims set forth below.

Brief Description of the Figures

25 Figure 1 shows the hypervariable region of a number of illustrative AT domains. Figure 2 shows a diagram and products of three modular PKS systems.

Modes of Carrying Out the Invention

As discussed above, modular polyketide synthases (PKSs) are large 30 multifunctional enzyme complexes that are organized into modules, where in addition to a loading domain in the first module, each module carries the domains needed to catalyze the condensation of an extender unit onto a growing polyketide chain. For example, the modular polyketide synthase, 6-deoxyerythronolide B synthase (DEBS), from

Saccharopolyspora erythraea is an assembly of three large multifunctional proteins - DEBS1, DEBS2, and DEBS3 - that catalyze the biosynthesis of the erythromycin macrolactone, 6-deoxyerythronolide B (6-dEB). Each of the three proteins is organized into two modules, and each module carries the catalytic domains needed to incorporate 5 one of six methylmalonyl-CoA extender units onto a growing polypropionate chain (see Cortés *et al.*, 1990, *Nature* 348: 176-178, and Donadio *et al.*, 1991, *Science* 252: 675-679, each of which is incorporated herein by reference). The modular polyketide synthases in general share this organization. Additional examples of such modular PKS include those which synthesize the macrolactone precursors for picromycin, oleandomycin, epothilone, 10 narbomycin, FK-520 and rapamycin. Significant portions of these and other modular PKS have been cloned and sequenced.

It will be evident that the nature of the macrolactone produced will depend on the number of modules in the PKS system, the nature of the starter and of the extender unit added by each module, and, if the extender unit results in a chiral center, the 15 stereochemistry resulting from the condensation or further reaction. The ability to manipulate the PKS genes, both in cell-free systems and in cells transformed with recombinantly manipulated DNA, permits ready control of the number of modules present. In addition, it has been possible to mix and match domains and modules from existing PKS genes to generate novel polyketides. See, for example Khosla, 1997, *Chem. Rev.* 97: 2577-2590; Hopwood, 1997, *Chem. Rev.* 97: 2465-2495; Shen *et al.*, 1995, *J. Amer. Chem. Soc.* 117: 6811-6821; and PCT publication Nos. WO 99/03986 and 20 97/02358, each of which is incorporated herein by reference. See, also, U.S. Patent No. 5,672,491.

The present invention provides a more focused approach to controlling the nature 25 of the starter and extender units incorporated, and expands the range of starter and extender unit candidates for incorporation. It also provides extender substrates which can be economically synthesized for incorporation into novel polyketides. These extender substrates include not only those which are incorporated by naturally occurring PKS enzymes, but also "unnatural" extender units which are incorporated only by virtue of 30 manipulation of the PKS genes according to the methods of the present invention. In addition, the invention provides a means to control the stereochemistry of the chiral centers in the resulting polyketide.

Extender Unit Variation and Incorporation

Several recent studies have demonstrated that extender unit specificity can be altered by AT domain substitution, and it is well-established that the extender-unit specificity towards malonyl- or methylmalonyl-CoA is exclusively controlled by the AT domains of the individual modules. It is also known that when methylmalonyl-CoA is the extender unit, only the (2S)-methylmalonyl-CoA enantiomer is incorporated. The present invention has resulted in the identification of an "AT hypervariable region" that controls the acceptance of starter and extender units. As further described below, the AT domain, while controlling the stereochemistry of the extender unit accepted, does not control the resulting chirality of the condensation product.

With regard to the role of AT domains in controlling the nature of extender units, it has been shown that replacement of the AT1 domain of DEBS1+TE with the RAPS AT2 domain results in biosynthesis of the predicted 4-desmethyl-triketide lactone (see Oliynyk *et al.*, 1996, *Chem. & Bio.* 3: 833-839, incorporated herein by reference). Similarly, replacement of the individual AT1, AT2, or AT6 domain of DEBS with heterologous AT domains that are specific for malonyl-CoA leads to production of the predicted desmethyl 6-dEB or erythromycin derivative (see Ruan *et al.*, 1997, *J. Bact.* 170: 6416-6425; and Liu *et al.*, 1997, *J. Am. Chem. Soc.* 119: 10553-10554, each of which is incorporated herein by reference).

However, the yields of the products generated by these chimeras vary greatly depending on the position of the polyketide chain at which the modified extender unit is incorporated. For example, production of the 10-desmethylerythromycin derivatives, resulting from replacement of the DEBS AT2 domain with a heterologous AT domain specific for malonyl-CoA, is significantly lower than that of the 12-desmethylerythromycin derivative, which results from replacement of the DEBS AT1 domain with a malonyl-CoA-specific AT domain (see Ruan *et al.*, 1997, *supra*). This suggests that intermediates that are altered at different positions of the polyketide backbone, may be recognized or processed to varying degrees by the modules downstream of the one responsible for the modification. Liu *et al.* 1997, *supra* also report that replacement of the final AT domain of DEBS (AT6) with the malonyl-CoA-specific RAPS AT2 domain leads to sizable production of the 2-desmethyl-6-dEB compound. In this case the resulting modified intermediate generated by module 6 does not have to undergo further downstream processing and can simply be directly cyclized by the thioesterase domain.

Sequence analysis of 20 AT domains from DEBS and RAPS led to the identification of signature sequences that could be used to discriminate between malonyl transferases and methylmalonyl transferases (see Haydock *et al.*, 1997, *FEBS* 374: 246-248, incorporated herein by reference). Subsequent studies on the FK-506, rifamycin, and niddamycin (see Motamedi *et al.*, 1997, *Eur. J. Biochem.* 224: 74-80; August *et al.*, 1998, *Chem. & Biol.* 5: 69-79; and Kakavas *et al.*, 1997, *J. Bact.* 179: 7515-7522, each of which is incorporated herein by reference) PKSs have confirmed that the utility of these signature sequences in analyzing naturally occurring PKS modules. The predictive power of these signature sequences is probably due to evolutionary constraints rather than mechanistic ones. The signature sequences are at a location in the AT domains different from that of the hypervariable region described below. They appear to be of diagnostic use only, and are not causative of specificity. Thus, whereas the *a priori* prediction of substrate specificity of AT domains found in nature can benefit from the above-mentioned signature sequences, the design of AT domains with altered or relaxed substrate specificity will require structure-based and/or combinatorial genetic manipulation of the hypervariable region in accordance with the methods of the present invention.

The structural determinants of extender specificity in the AT domains were identified by the present inventors by constructing hybrid AT domains. Fragments of a malonyl-CoA-specific AT domain were replaced with homologous segments from a methylmalonyl-CoA-specific AT domain, and vice versa. Specifically, replacement of the DEBS AT2 domain by the RAPS AT2 domain in DEBS1+TE leads to the production of approximately 10 mg/mL of the expected 2-desmethyl triketide lactone. By contrast, the same domain swap in the full (6-module) DEBS system results in a considerably lower yield of the corresponding 10-desmethyl 6-dEB (<1 mg/L). This finding supports the suggestion that the heterologous RAPS AT2 domain is fully capable of recruiting a malonyl-CoA extender unit for incorporation onto the growing polyketide chain, and that subsequent processing of the altered intermediate by downstream modules poses as the main obstacle to efficient product formation.

To dissect the role of specific amino acids in controlling AT substrate specificity, experiments were conducted in which several subdomains between selected malonyl- and methylmalonyl-transferases were exchanged. The results showed that a short (20-35 amino acid) C-terminal segment present in all AT domains is the principal determinant of

their substrate specificity. The length and amino acid sequence of this segment, varies considerably among the known AT domains and is thus defined herein as the AT "hypervariable region." The present inventors have discovered that the choice of extender units by the PKS modules is influenced by this "hypervariable region", which can be 5 manipulated by mutagenesis to generate novel AT domains possessing relaxed or altered substrate specificity.

To delineate the region of the AT domain that controls extender substrate specificity, a hybrid PKS which contains the RAPS AT2 domain in place of the DEBS AT2 domain in the full (6 module) DEBS system was used as a base. Then, a series of 10 chimeric AT domains were constructed by replacing fragments of this RAPS AT2 domain (which utilizes malonyl-CoA as substrate) with homologous regions from the DEBS AT2 domain (which uses methylmalonyl-CoA). These chimeric AT domains then were inserted in place of the RAPS AT2 domain. Most chimeras thus generated were apparently inactive.

15 In particular, a 120-bp *XbaI-SstI* fragment encoding the divergent signature sequence motif described above from the malonyl-CoA-specific RAPS AT2 domain was replaced by a 140-bp fragment encoding the signature sequence motif for the methylmalonyl-CoA-specific DEBS AT2 domain. The resulting recombinant strain did not produce detectable product. However, when a 190-bp *PinAI-PstI* fragment at the 3'- 20 end of the RAPS AT2 domain was replaced by a homologous 200-bp fragment from the 3'-end of the DEBS AT2 domain, the resulting recombinant strain produced approximately 10 mg/L of the 6-dEB macrolactone.

The 190-bp *PinAI-PstI* fragment at the 3'-end of the RAPS AT2 domain can be further subdivided into a 63-bp *NheI-StyI* fragment and a 120-bp *StyI-PstI* fragment. The 25 recombinant strain, in which the 120-bp RAPS *StyI-PstI* was replaced by the 110-bp DEBS *StyI-PstI* fragment in the full DEBS, did not generate any detectable polyketides. On the other hand, the recombinant strain, in which the 63-bp RAPS *NheI-StyI* fragment was replaced by the 99-bp DEBS *NheI-StyI* fragment in the full DEBS, produced about 10 mg/L of 6-dEB.

30 These results demonstrate that the *NheI-StyI* fragment plays an important role in controlling the substrate specificity of at least one AT domain. A reverse experiment whereby substitution of this segment in a methylmalonyl-AT domain by its counterpart from a malonyl-AT domain would lead to the formation of the expected desmethyl-

analog of the natural product was then conducted. As stated above, substitution of DEBS AT6 by RAPS AT2 leads to the biosynthesis of 2-desmethyl-6-dEB in good yield (10 mg/L). Therefore, module 6 of the DEBS was selected for the reverse experiment.

The 84-bp *NheI-StyI* fragment of the DEBS AT6 domain, which is homologous to 5 the 99-bp *NheI-StyI* fragment of the DEBS AT2 domain, was replaced by the 63-bp *NheI-StyI* fragment of the RAPS AT2 domain. The design of this hybrid was based on well-established sequence alignments of AT domains from modular PKSs. The resulting recombinant strain produced the predicted 2-desmethyl 6-dEB (~5 mg/L) as well as comparable amounts of 6-dEB. A mixture of the two compounds is also known to be 10 present in extracts from the recombinant strain previously described (see Liu *et al.*, 1997, *supra*).

Thus the 33 amino-acid segment encoded by the *NheI-StyI* fragment of the DEBS AT2 domain, or its counterparts in other AT domains, such as DEBS AT6 and RAPS AT2, are important determinants of specificity for methylmalonyl- or malonyl-CoA substrates. Sequence comparison among analogous segments from these and other 15 known AT domains reveals striking diversity both with respect to length (21-33 residues) and sequence. Illustrative representative sequences of these hypervariable domains are shown in Figure 1. While a definitive consensus sequence or sequences that universally correlate primary protein structure to substrate specificity cannot as yet be deduced, the 20 corresponding hypervariable region in any AT domain amino acid sequence can be identified by comparison with the illustrative sequences shown in Figure 1. Most remarkably, this region varies considerably from its counterpart in the crystallographically characterized malonyl transferase of the *E. coli* fatty acid synthase (see Serre *et al.*, 1995, *J. Biol. Chem.* 270: 12961-12964, incorporated herein by 25 reference). Based on an analogy with the immunoglobulins, the substrate specificity of AT domains in modular PKSs can be said to be controlled by a "hypervariable region" located at the C-terminal end of the domain, whose boundary can be defined from sequence comparison, as including 20-35 amino acid residues corresponding to the sequence encoded by the 99-bp *NheI-StyI* fragment of the DEBS AT2 domain.

30 Thus, the invention provides a suitable target "hypervariable region" identified in the AT domains of the modular PKS systems which can be manipulated to alter the specificity with respect to extender substrates so that the PKS system can incorporate not only other extenders which are incorporated into wild-type polyketides but also

permitting these domains to incorporate extender units which have heretofore not been incorporated into polyketides or are not incorporated into polyketides in native systems. In one aspect, the invention provides a method for altering the specificity of an acyltransferase domain of a polyketide synthase, which method comprises the step of

5 changing the amino acid sequence of the hypervariable region of the AT domain without changing at least a portion of the remaining AT domain amino acid sequence so that the specificity of the AT domain is changed from one naturally occurring starter or extender unit to another. In this embodiment, the known sequences of AT domains with the desired alternative specificity may be used as a guide. In a related embodiment, the

10 invention provides a method for changing the specificity of an AT domain of a PKS to accommodate a starter or extender unit not normally incorporated by a PKS. This method also comprises altering the amino acid sequence of the hypervariable region of the AT domain, for example, by specific or random mutagenesis. In this embodiment, the method optionally further comprises contacting the PKS comprising the altered AT

15 domain with one or more non-naturally incorporated starter or extender units, and identifying whether the altered AT domain can incorporate the tested incorporated starter or extender unit. In related embodiments, the invention provides novel PKS enzymes capable of incorporating non-naturally incorporated starter or extender unit, methods of using them, and novel polyketides produced thereby.

20 The amino acid sequence of the hypervariable region of an AT domain can be altered by a variety of methods known in the art. If desired, the amino acid sequence may be altered at the protein level by suitable synthesis methods. However, it is much more convenient and efficient to modify the nucleotide sequence encoding the hypervariable region. This can be done either in the context of a fragment of DNA containing only the

25 nucleotides of the hypervariable region, or may be performed on larger portions of the AT domain, the module in which it is contained, or in the context of the entire PKS.

Individual modules of a PKS system may be modified so that a variety of extender units is incorporated into the polyketide. Thus, it would be possible to modify the

30 hypervariable regions in the DEBS PKS in only selected modules such as modules 2, 5 and 6 to the exclusion of modifications in the remaining modules. The specificity of each individual AT domain can thus be controlled.

Having constructed a PKS of an arbitrary number of modules with the required specificity, polyketides may be produced conveniently either in a cell-free system or in a

recombinantly transformed host by supplying the appropriate starter and extender substrates. In some cases, of course, the substrates will already be present in a host cell; in other cases, it will be necessary to supply them for purposes of the production of the polyketide. Described hereinbelow is a cost effective method to prepare useful substrates 5 to generate the extender units both in cases where the extender unit is naturally incorporated by at least one wild-type PKS and in cases where an extender unit is not found in naturally occurring polyketides.

Methods and Compositions for Providing Extender Units

10 In another embodiment, the present invention provides non-naturally occurring extender substrates for PKS enzymes and methods of making them. In one embodiment, these non-naturally occurring extender substrates are used to make polyketides in a cell-free system and in host cells that do not naturally produce polyketides but which can produce polyketides when provided with a recombinant PKS and one or more novel 15 extender units of the invention.

The extender substrates provided by the invention may result in the incorporation of a subunit normally included in a polyketide made by a wild-type PKS, or may provide for the incorporation of a subunit that is not natively incorporated into any polyketide.

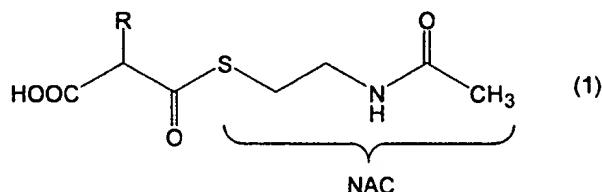
20 The naturally occurring substrates for both starter and extender subunits are typically coenzyme A thioesters of the relevant carboxylic acids. However, the cost of the required coenzyme A thioesters needed for chain extension is prohibitive to larger scale *in vitro* synthesis of polyketides or simple *in vivo* synthesis in organisms such as *E. coli* that do not naturally synthesize an endogenous supply of the required extender 25 substrate MeMalCoA. A less costly extender unit is key to the realization of preparative scale syntheses of engineered polyketides.

It has been shown that a truncated form of the coenzyme A thioester of a diketide can be incorporated into the growing polyketide chain by modular PKS systems. (See, for example, European application 96/925275.8 and PCT application PCT/US98/14911. This is consistent with the finding that the N-acetyl cysteamine (NAC) thioesters can be 30 incorporated both *in vivo* and *in vitro* as primers for polyketide synthesis (see Yue *et al.*, 1987, *J. Amer. Chem. Soc.* 109: 1253-1257, incorporated herein by reference). These analogs can be taken up by cells from exogenous media, unlike CoA esters, and can be accepted by the desired PKS enzymes. However, whether the time scale of iterative

condensations versus initial priming would allow incorporation of extender NAC-thioester substrates was unclear prior to the present invention.

Further, the preparation even of the NAC thioester of methyl malonic acid has not been reported. Malonyl NAC thioester has been described, but without description of its preparation method (see Arnstadt, 1976, *Liebigs Ann. Chem.*, 1976: 843-847, incorporated herein by reference). While the multistep route used to make methylmalonyl coenzyme A (MeMalCoA) via the thiophenyl ester (see Padmakumar *et al.*, 1993, *Anal. Biochem.* 214: 318-320, incorporated herein by reference) should be able to produce the NAC analog, a shorter sequence in which the difficult monothioesterification of a diacid could be avoided is desirable. The present invention provides such a method which is applicable to extender substrates in general.

Thus, the invention provides extender substrates which are N-acetyl cysteamine thioesters of the formula:



i.e., HOOC-CHR-CONAC (1),

wherein R is alkyl (1-8C), alkenyl (1-8C) or alkynyl (1-8C) optionally containing one or more heteroatoms, and optionally substituted with one or more substituents selected from the group consisting of halo, -OR', -SR' and -NR'₂, wherein each R' is independently H or alkyl (1-6C) and wherein the substitution is nontoxic to the PKS enzyme. The alkyl, alkenyl, and alkynyl substituents may be straight-chain, branched or cyclic.

R may also be aryl (6-10C), heteroaryl (6-10C) wherein the aromatic system contains one or more nitrogens, or is arylalkyl (7-15C) or heteroarylalkyl (7-15C). These embodiments of R may be substituted as described for the alkyl, alkenyl and alkynyl moieties set forth above. In addition, the aryl and heteroaryl moieties may be substituted by additional alkyl, alkenyl or alkynyl groups in all cases (1-8C) as described above. The substitution in such cases must also be nontoxic to the PKS enzyme.

Preferred embodiments of the compound of formula (1) are those wherein R is lower alkyl (1-4C), lower alkenyl (1-4C) or lower alkynyl (1-4C) optionally substituted with one or two substituents selected from the group set forth above except that each R' is

independently H, methyl or ethyl. Also preferred are embodiments wherein R is substituted or unsubstituted phenyl, benzyl, phenylethyl or phenylpropyl. Substitution of these embodiments of R is preferably one or two substituents on the phenyl moiety which are halo, -OH, -OCH₃, -NH₂, -NHCH₃, -N(CH₃)₂ or lower alkyl (1-4C). Where R

5 includes a heteroaryl moiety, preferred embodiments include pyridine pyrimidine, indole, quinolyn and azulene. Where R is alkyl, alkenyl or alkynyl containing one or more heteroatoms, preferred heteroatoms are O and N and among these, preferred embodiments are cyclic. Thus, preferred embodiments include substituted or unsubstituted cyclohexyl, cyclopentyl, piperidine, piperazine, furan, tetrahydrofuran, and the like.

10 Especially preferred among compounds of formula (1) are those embodiments wherein R is an unsubstituted alkyl, alkenyl, alkynyl, aryl or arylalkyl, most preferably unsubstituted lower alkyl, lower alkenyl, lower alkynyl, phenyl, benzyl, phenylethyl or phenylpropyl. Also preferred are unsubstituted alkyl, alkenyl, or alkynyl containing one or more heteroatoms or unsubstituted heteroaryl or heteroarylalkyl.

15 The compounds of formula (1) contain a chiral center. Accordingly, the invention is directed to compounds of formula (1) which may be in the form of racemic mixtures or may be in the form of an isolated enantiomer. Because the AT domains in the PKS systems may be manipulated to relax their substrate specificities, both the R and S forms of the compound of formula (1) are included in the invention. Further, the substituent R

20 may itself contain chiral centers and thus various forms of the compound of formula (1) with respect to its stereoisomers are within the scope of the invention. The invention includes compounds of formula (1) having varying amounts of individual stereoisomers of that formula.

To prepare the compounds of formula (1), Meldrum's acid or an analog thereof is

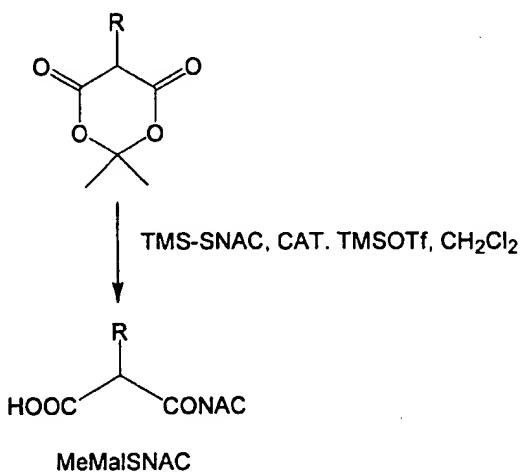
25 used as a starting material. Meldrum's acid is a commonly used substrate for acylation chemistry, because nucleophilic ring-opening and decarboxylation subsequently yields beta-keto esters (see Oikawa *et al.*, 1978, *J. Org. Chem.* 43: 2087-2088, and Gilbert *et al.*, 1995, *Biorg. Med. Chem. Lett.* 5: 1587-1590, incorporated herein by reference). Direct nucleophilic attack of Meldrum's acid is a common route to various monoesters (see

30 McNab, 1978, *Chem. Soc. Rev.* 7: 345-358, incorporated herein by reference).

Surprisingly, treatment of methyl Meldrum's acid with NAC failed to afford the desired thioester. A more reactive nucleophile is required, but the low pKa (4.97; see Pihlaja *et*

al., 1969, *Acta Chem. Scand.* 23: 3003-3010, incorporated herein by reference) of Meldrum's acid prohibited use of preformed thiolates.

Previous work with amines and alcohols (see Rigo *et al.*, 1989, *Tetrahedron Lett.* 30: 3073-3076, incorporated herein by reference) suggested that silylated nucleophiles 5 would permit milder conditions. A trimethylsilylated thiol nucleophile made with catalytic trimethylsilyl triflate (see Sassaman *et al.*, 1990, *Synthesis* 1990: 104-106, incorporated herein by reference) was effective without addition of heat. Both Meldrum's acid and methyl Meldrum's acid were converted to the desired NAC thioesters by treating the starting material with N-acetyl cysteamine in the presence of a 10 trimethylsilyl catalyst in methylene chloride as shown below:



MeMalSNAC

When R is methyl, the data verifying the product are as follows:

^1H NMR (400 MHz, CDCl_3) delta 9.50 (br s, 1 H), 6.41 (br s, 1 H), 3.63 (q, $J = 7.0$ Hz, 1 H), 3.42-3.34 (m, 2 H), 3.11-2.93 (m, 2 H), 1.99 (s, 3 H), 1.45 (d, $J = 7.0$ Hz, 3 H); ^{13}C NMR (100 MHz, CDCl_3) delta 197.7, 172.8, 172.7, 54.8, 40.1, 29.2, 23.4, 14.7; 15 FAB $^+$ MS (NBA/NaI) calcd. for $(\text{C}_8\text{H}_{12}\text{O}_4\text{N}_2)\text{H}^+$ 220.0644, observed 220.0641).

Incorporation of NAC Thioesters

On a per mole basis, MeMalSNAC is about 4000 times cheaper than the 20 corresponding coenzyme A derivative. (Actually, methyl Meldrum's acid is less expensive per mole than methyl malonic acid.) However, only a five to ten-fold increase in concentration over usual MeMalCoA concentrations (1 mM) was needed to produce approximately the same amount of polyketide product.

MeMalSNAC was used in a reaction with the purified third polypeptide of DEBS (DEBS3 + TE). A doubly ^{13}C -labeled diketide (see Cane *et al.*, 1993, *J. Amer. Chem. Soc.* **115**: 522-526, incorporated herein by reference) was employed as a primer so that product formation could easily be identified by ^{13}C NMR. In fact ^{13}C NMR of the crude 5 ethyl acetate extract of the enzymatic reaction clearly showed formation of the known triketide lactone, thereby confirming the acceptance of MeMalSNAC as a substrate by the DEBS3 + TE system. In addition to the doubly ^{13}C -labeled unincorporated diketide showing two strong doublets, two doublets with 35 Hz coupling could also be seen that were shifted to the characteristic lactone chemical shifts. The coupling constants 10 remained the same upon going to a higher field strength NMR, thereby ruling out assignment of these peaks to fortuitous singlets coming from large impurities.

Control of Stereochemistry

In 6-dEB, the stereochemistry of the methyl-branched centers arising from the 15 individual condensation reactions is also determined as each successive C_3 unit is added. In 6-dEB, the three chiral carbons at the C-2, C-4, and C-10 positions all have the D-methyl configuration, whereas those at the C-6, C-8, and C-12 positions have the L-methyl configuration. The D-methyl configuration is that which would result as expected from the D-carboxylative inversion of the (2S)-methylmalonyl CoA substrates, 20 which are required. The (2R)-methylmalonyl CoA enantiomer is not incorporated. (See Marsden *et al.*, 1994, *Science* **263**: 378-380, incorporated herein by reference.) Thus, the pattern observed in the DEBS system is as shown in the table below.

D-methyl	Generated by molecule		Generated by molecule	
	L-methyl	D-methyl		
C-2	6		C-12	1
C-4	5		C-8	3
C-10	2			

25 The present invention provides means to control the stereochemistry at these positions or positions where the chirality is controlled by the PKS in other polyketides.

It has been suggested that the PKS system itself is responsible for controlling the stereochemistry at most chiral centers. It has now been found that the AT domains of DEBS do not influence epimerization of the (2S)-methylmalonyl-CoA extender units, and that stereochemical control of the methyl-branched centers generated by DEBS resides in

the ketosynthase (KS) domains of the individual modules. The stereochemistry of a polyketide may therefore be controlled by including in the PKS the KS domains that dictate the desired stereochemistry. For example, recombinant PKS enzymes in which a KS domain specifying a first stereochemistry may be replaced by a KS domain specifying a second stereochemistry.

5 Certain parameters with respect to control of the polyketide stereochemistry are known. Incorporation of deuterated propionate into erythromycin A demonstrated that formation of the D-methyl centers at C-2, C-4, and C-10 of the polyketide chain results directly from decarboxylative inversion of the (2S)-methylmalonyl-CoA substrates (see
10 Cane *et al.*, 1986, *J. Am. Chem. Soc.* 108: 4957-4964, incorporated herein by reference). In the triketide lactone formed by DEBS1+TE, in the presence of (2S)-[2-²H]-methylmalonyl-CoA, H was lost from the C-4 position. The C-4 position in the triketide lactone carries the L-methyl center generated by module 1 corresponding to C-12 in 6-dEB (see Weissman *et al.*, 1997, *Biochemistry* 36: 13849-13855, incorporated herein by
15 reference).

20 Together, these findings suggest that generation of the L-methyl centers may involve an epimerization step that is catalyzed by DEBS itself. Because construction of the polyketide chain is processive, this epimerization step would have to take place either in the methylmalonyl moiety prior to the condensation step or in the polyketide product immediately following the ketosynthase reaction. Additional evidence bearing on the timing of the epimerization reaction comes from the recent finding that the
25 stereochemistry of beta-ketoreduction is an intrinsic property of the relevant ketoreductase (KR) domains and is independent of both the stereochemistry and the degree of substitution adjacent to the beta-keto group that undergoes reduction (see Kao *et al.*, 1998, *J. Am. Chem. Soc.* 120: 2478-2479, incorporated herein by reference).

30 If epimerization were indeed to occur before condensation, it is conceivable that the relevant acyltransferase domains (AT) of DEBS might epimerize the enzyme-bound (2S)-methylmalonyl group to the requisite (2R)-methylmalonyl diastereomer prior to the ketosynthase-catalyzed condensations that generate the beta-ketoacyl polyketide intermediates with L-methyl groups in the alpha-position. Although (2S)-methylmalonyl CoA serves as the sole substrate for the AT domains of DEBS, the expected D-methyl center, generated by decarboxylative inversion of the extender units, is found only in the growing polyketide chains produced by modules 2, 5, and 6. By contrast, the epimeric

L-methyl configuration is observed at C-12 and C-8, positions in the erythromycin polyketide generated by modules 1 and 3, respectively. Because the L-methyl configuration at the alpha position of the acyl chain generated by module 4 is certainly due to the reduction of its corresponding alpha-methyl-alpha, beta-unsaturated ester intermediate, it is unknown whether module 4 contains epimerase activity. Notwithstanding this ambiguity, the possible ability of the AT4 domain to epimerize its bound (2S)-methylmalonyl substrate can still be evaluated by alternately replacing the AT1 or AT2 domain of the DEBS1+TE mutant with the AT4 domain. If the AT4 domain were to have no intrinsic epimerase activity, then both of the derived hybrid PKSs would produce the natural (2R, 3S, 4S, 5R)-2,4-dimethyl-3,5-dihydroxy-n-heptanoic acid delta-lactone. On the other hand, if the donor AT4 domain, or one or the other of the replaced AT1 and AT2 domains were able to mediate epimerization, then one of the two hybrid PKSs would be expected to produce a diastereomer.

To test this hypothesis, two chimeric derivatives of DEBS1+TE, in which the AT domains of module 1 (AT1) and of module 2 (AT2) were independently replaced by the AT domain of module 4 (AT4) were constructed. Heterologous expression of DEBS1+TE in *Streptomyces coelicolor* normally results in formation of the triketide (2R, 3S, 4S, 5R)-2,4-dimethyl-3,5-dihydroxy-n-heptanoic acid delta-lactone (see Cortés *et al.*, 1995, *Science* 268: 1487-1489, and Kao *et al.*, 1995, *J. Am. Chem. Soc.* 117: 9105-9106, each of which is incorporated herein by reference). Each of the chimeric proteins, in which either AT1 or AT2 was replaced by AT4, produces the same triketide lactone with unaltered stereochemistry.

From these results, the observed interchangeability of DEBS AT4 with either the AT1 or the AT2 domain in formation of the triketide lactone suggests not only that the donor AT domain retains its catalytic activity upon introduction into another module, but that there is no intrinsic epimerase activity associated with any of these three AT domains. This is consistent with recent reports that replacement of the DEBS KR2 domain with either the KR2 or KR4 domains of the rapamycin PKS results in formation of the 3-epi-triketide lactone, thereby establishing that the configuration of the polyketide hydroxyl groups is controlled directly by the operative KR domain and is not correlated with the stereochemistry or degree of substitution at the adjacent alpha-position (see Kao *et al.*, 1998, *J. Am. Chem. Soc.* 120: 2478-2479, incorporated herein by reference). It has also been shown that replacement of the DEBS ACP3 domain with the DEBS ACP6

domain in a truncated trimodular PKS does not result in alteration of stereochemistry of the relevant methyl-branched centers (see McDaniel *et al.*, 1997, *Chem. & Biol.* 4: 667-674, incorporated herein by reference). Thus, neither the AT, the KR, nor the ACP domain is responsible for the epimerization that results in generation of the L-methyl-
5 branched centers derived from (2S)-methylmalonyl-CoA. The critical epimerase activity is therefore associated directly with the individual KS domains.

It has thus been found that the stereochemistry of the methyl-branched centers of 6-dEB and the corresponding branched centers of other polyketides is controlled by the KS domains of the corresponding modules for those centers. It is thus possible to alter
10 the stereochemistry of a polyketide by modifying the PKS that produces the polyketide to replace a KS domain specifying an undesired stereochemistry with another KS domain that specifies an alternate stereochemistry.

Thus, with respect to the DEBS PKS system, it is clear that the KS1 and KS3 ketosynthase domains will result in an "L-methyl" or corresponding configuration of a
15 polyketide formed from a substituted malonate and KS2, KS5 and KS6 will result in the alternative stereochemistry. In constructing polyketides or libraries thereof, therefore, it is possible to use this information to control the stereochemistry of any position generated from an extender unit containing a chiral center at the α -position (unless the stereochemistry is controlled by reduction of a π -bond as is the case for the
20 stereochemistry at C-6 in DEB). Thus, for any length module PKS, with any choice of extender units, the number of possible variants is enhanced by 2 raised to the power of the number of chiral centers that can be specified in this way. Specifically, for example, the stereochemistry at C-12 of 6-DEB can be altered from the L-methyl configuration to the D-methyl configuration by replacing KS1 with, for example, KS5 of the same PKS
25 system.

The following examples are given for the purpose of illustrating the present invention and should not be construed as limiting the scope of the invention or claims.

30

Example 1Plasmid Construction

The plasmid pCK7 contains the complete DEBS gene cluster shown in Figure 2; plasmid pCK12 contains the genes encoding DEBS1+TE. (See Kao *et al.*, 1995, *J. Am.*

*Chem. Soc. 11: 9105-9106, and Kao et al., 1994, J. Am. Chem. Soc. 116: 11612-11613, U.S. Patent No. 5,672,491, all of which are incorporated herein by reference). Plasmids pJL130 and pJL008 are each derivatives of pCK12 in which a 1.0-kb *BamHI-PstI* fragment corresponding to either the AT1 domain or the AT2 domain, respectively, is replaced by a 1.0-kb *BamHI-PstI* fragment corresponding to the AT4 domain of DEBS. pKOS008-51 and pJL185 are, respectively, derivatives of pCK12 and pCK7 in which the 1.0-kb *BamHI-PstI* fragment corresponding to the entire AT2 domain of DEBS is replaced with a 0.9-kb *BglII-PstI* fragment corresponding to the intact AT2 domain of the rapamycin polyketide synthase (RAPS).*

10 Plasmid pJL286 is a derivative of pJL185, in which a 120-bp *XhoI-SstI* fragment of the RAPS AT2 domain encoding the sequence motif suggested to be responsible for malonyl-CoA specificity is excised and replaced with an analogous fragment from the DEBS AT2 domain encoding the corresponding sequence motif suggested for methylmalonyl-CoA specificity (see Haydock et al., 1997, *FEBS* 374: 246-248, incorporated herein by reference).

15 Plasmid pJL259 is a derivative of pJL185, in which a 190-bp *PinAI-PstI* fragment encoding the C-terminal region of the RAPS AT2 domain is excised and replaced with its homologous counterpart from the DEBS AT2 domain. Plasmids pJL285 and pJL287 are also derivatives of pJL185, in which either a 63-bp *NheI-StyI* fragment or a 120-bp *StyI-PstI* fragment corresponding to a subregion of the RAPS *PinAI-PstI* fragment, respectively, is replaced with its counterpart from the DEBS AT2 domain. Plasmid pJL305 is a derivative of pCK7 in which a 84-bp *NheI-StyI* fragment encoding a subregion of the DEBS AT6 domain that is homologous to the one encoded by the *NheI-StyI* fragment of the DEBS AT2 domain, is replaced with the 63-bp *NheI-StyI* fragment of the RAPS AT2 domain.

20 The table below summarizes the plasmids that were described in the preceding paragraph.

Derived from pCK12 (DEBS1 + TE)	
pJL130	AT1 → AT4
pJL008	AT2 → AT4
pKOS008-51	AT2 → AT2 (RAPS)
Derived from pCK7 (DEBS-6 modules)	
pJL185	AT2 → AT2 (RAPS)
pJL305	AT2 → AT2/AT6 (63bp <i>NheI/StyI</i>)

Derived from pJL185 (DEBS - 6 modules)	
pJL286	AT2 (RAPS) → replace 120bp XbaI/SstI
pJL259	AT2 (RAPS) → replace 190bp PstI/PstI
pJL285	AT2 (RAPS) → 63bp NheI/StyI
pJL287	AT2 (RAPS) → 120bp StyI/PstI

Each of these plasmids was introduced into *S. coelicolor* CH999 (see U.S. Patent No. 5,672,491, incorporated herein by reference) via transformation, and the polyketide products were purified from the resulting transformants according to methods previously 5 described (see Kao *et al.*, 1994, *J. Am. Chem. Soc.* 116: 11612-11613, incorporated herein by reference).

Example 2

Analysis of Recombinant Strains

10 The recombinant strains, CH999/pJL130 and CH999/pJL008, both synthesized a triketide identical to that produced by the parent DEBS1+TE strain. The stereochemistry of the products was established by ¹H NMR spectroscopy and comparison of the data with that for authentic compound.

15 The recombinant strain, CH999/pKOS008-51 produced 2-desmethyl-triketide lactone. This novel metabolite was produced at ~10 mg/L, which is half that of the production levels of the parent triketide lactone (~ 20 mg/L). The structure of this product was confirmed by ¹H and ¹³C NMR spectroscopy.

20 Similarly, the recombinant strain, CH999/pJL185 putatively produced 10-desmethyl 6-dEB, however, this was generated in amounts insufficient for exhaustive spectroscopic characterization (<1 mg/L). Its existence in the fermentation broth was detected by AP-Cl mass spectroscopy ($M + H^+ = 373$, $M - H_2O + H^+ = 355$, $M - 2H_2O + H^+ = 337$). This result is consistent with that described in Ruan *et al.*, 1997, *J. Bact.* 170: 6416-6425 where the corresponding 10-desmethyl analog of erythromycin was produced by similar AT swaps into DEBS in the native erythromycin producer *Saccharopolyspora erythraea*. Although the exact titers were not reported, Ruan *et al.* reported the isolation of a few milligrams of the product from a 27 L fermentation, suggesting that the titer of this novel erythromycin in *S. erythraea* was considerably lower than that of the parent natural product in the same host. (This is shown diagrammatically in Figure (2).)

The recombinant strains, CH999/pJL286, CH999/pJL259, CH999/pJL285, and CH999/pJL287, contained hybrid RAPS/DEBS AT2 domains. Of the four mutants, CH999/pJL286 and CH999/pJL287 did not produce any detectable polyketides. CH999/pJL259 and CH999/pJL285 both produced approximately 10 mg/L of the 6-dEB 5 macrolactone. The structure of this product was again confirmed by ^1H NMR spectroscopy. No 10-desmethyl-6-dEB could be detected.

Likewise, the recombinant strain, CH999/pJL305 which carries a plasmid where the AT6 domain of the 6-module DEBS system was replaced with a chimeric DEBS/RAPS domain produced both 6-dEB and the 2-desmethyl 6-dEB in comparable 10 amounts (~ 5 mg/L). The structures were also confirmed by ^1H NMR.

The invention having now been described by way of written description and examples, those of skill in the art will recognize that the invention can be practiced in a variety of embodiments and that the foregoing description and examples are for purposes of illustration and not limitation of the following claims.

Claims

1. A method to alter the specificity of a module of a modular polyketide synthase with respect to its ability to incorporate a starter or extender unit into a polyketide which method comprises modifying the amino acid sequence of the hypervariable region of the acyltransferase (AT) domain of said module so as to change said specificity.
5
- 10 2. The method of claim 1 wherein said modifying comprises mutagenizing the nucleotide sequence encoding said hypervariable region.
- 15 3. The method of claim 1 wherein said modifying comprises replacing all or a portion of said hypervariable region with an alternative amino acid sequence without replacing the entire AT domain.
- 20 4. The method of claim 1 wherein said altered specificity is characterized by the ability of said module to accept more starter or extender units than accepted by said module in unmodified form.
- 25 5. The method of claim 1 wherein the specificity is altered so as to accept a starter or extender unit which is natively accepted by a module from a different naturally occurring PKS.
- 30 6. The method of claim 5 wherein the specificity is altered from accepting acetyl as a starter unit to accepting propionyl as a starter unit or vice-versa.
7. The method of claim 6 wherein the amino acid sequence of the hypervariable domain is changed from that of DEBS to that of NID or vice-versa.
8. The method of claim 5 wherein the specificity is altered with respect to an extender unit.

9. The method of claim 8 wherein the specificity is altered so as to provide the ability to accept methylmalonyl, ethylmalonyl, or malonyl extender units to a module lacking such ability.

5 10. The method of claim 9 wherein the hypervariable region amino acid sequence is altered to accept said units by providing the amino acid sequences required for such acceptance as set forth in Figure 1.

11. The method of claim 1 wherein said altered specificity results in the ability 10 of said module to accept a starter or extender unit not incorporated into a polyketide by a naturally occurring PKS.

12. The method of claim 11 wherein said extender unit is derived from a malonic acid ester and said unit is of the formula -RCHCO-
15 wherein R is alkyl (1-8C), alkenyl (1-8C), alkynyl (1-8C) optionally containing one or more heteroatoms, or is aryl (6-10C), heteroaryl (6-10C), arylalkyl (7-15C) or heteroarylalkyl (7-15C) each of the foregoing either substituted or unsubstituted with one or more substituents selected from the group consisting of halo, -OR', -SR' and -NR'₂ wherein each R' is independently H or alkyl (1-6C) or wherein said aryl or heteroaryl 20 moieties may be substituted with one or more alkyl, alkenyl, or alkynyl, with the proviso that -RCHO- is not incorporated into a polyketide by a naturally occurring PKS.

13. The method of claim 12 wherein R is lower alkyl (1-4C), lower alkenyl (1-4C) or lower alkynyl (1-4C) optionally substituted with one or two substituents 25 selected from the group consisting of halo, -OR', -SR' and -NR'₂, wherein each R is independently H, methyl, or ethyl.

14. The method of claim 12 wherein R is phenyl, benzyl, phenylethyl or phenylpropyl unsubstituted or substituted with one or two substituents on the phenyl 30 moiety which are halo, -OH, -OCH₃, -NH₂, -NHCH₃, -N(CH₃)₂ or lower alkyl (1-4C).

15. The method of claim 12 wherein R is unsubstituted alkyl, alkenyl, or alkynyl each optionally containing one or more heteroatoms or is unsubstituted heteroaryl or heteroarylalkyl.

5 16. The method of claim 11 wherein said extender unit is supplied as a substrate which is a thioester of a malonic acid derivative.

17. The method of claim 16 wherein the thioester is a Co-enzyme A thioester or a N-acetyl cysteamine thioester.

10

18. The method of claim 11 wherein the starter unit is of the formula RCH₂CO- wherein R is as defined in claim 12.

15 19. The method of claim 11 which further comprises contacting the module with a substrate that supplies said starter or extender unit and determining the incorporation of said unit.

20 20. A method to produce a polyketide which method comprises contacting a PKS containing a module modified according to the method of claim 1 with starter and extender substrates accepted by said PKS.

21. The method of claim 20 wherein said contacting is in a cell-free system.

25 22. The method of claim 20 wherein said contacting is accomplished by culturing cells which contain a PKS comprising a module modified by the method of claim 1.

23. A polyketide produced by the method of claim 20.

30 24. A method to alter the chirality imposed by a polyketide synthase module on an extender unit included in a polyketide which method comprises substituting for the ketosynthase (KS) domain of said module a KS domain which imposes the opposite chirality.

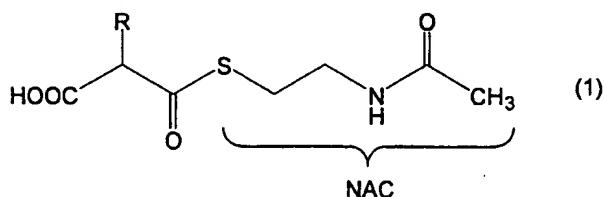
25. The method of claim 24 wherein a KS domain that directs decarboxylative inversion of a chiral malonyl substrate is substituted for a KS domain that effects epimerization to the opposite chirality or vice-versa.

5

26. A method to produce a polyketide of desired chirality at at least one chiral center which method comprises contacting a PKS modified by the method of claim 24 with starter and extender substrates.

10

27. A synthetic extender unit of the formula



15

wherein R is alkyl (1-8C), alkenyl (1-8C), alkynyl (1-8C) optionally containing one or more heteroatoms, or is aryl (6-10C), heteroaryl (6-10C), arylalkyl (7-15C) or heteroarylalkyl (7-15C) each of the foregoing either substituted or unsubstituted with one or more substituents selected from the group consisting of halo, -OR', -SR' and -NR'₂ wherein each R' is independently H or alkyl (1-6C) or wherein said aryl or heteroaryl moieties may be substituted with one or more alkyl, alkenyl, or alkynyl, with the proviso that RCHO is not incorporated into a polyketide by a naturally occurring PKS.

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28. The extender unit of claim 27 lower alkyl (1-4C), lower alkenyl (1-4C) or lower alkynyl (1-4C) optionally substituted with one or two substituents selected from the group consisting of halo, -OR', -SR' and -NR'₂, wherein each R is independently H, methyl, or ethyl.

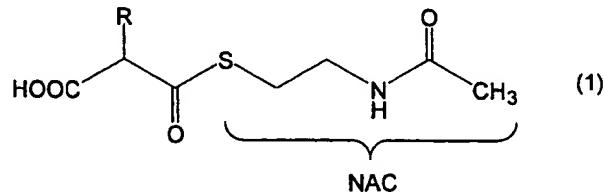
25

29. The extender unit of claim 27 wherein R is phenyl, benzyl, phenylethyl or phenylpropyl optionally substituted with one or two substituents on the phenyl moiety which are halo, -OH, -OCH₃, -NH₂, -NHCH₃, -N(CH₃)₂ or lower alkyl (1-4C).

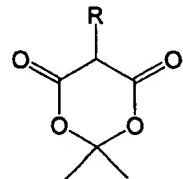
30. The extender unit of claim 27 wherein R is unsubstituted alkyl, alkenyl, or alkynyl each optionally containing one or more heteroatoms or is unsubstituted heteroaryl or heteroarylalkyl.

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31. A method to prepare a synthetic extender unit of the formula



wherein R is alkyl (1-8C), alkenyl (1-8C), alkynyl (1-8C) optionally containing one or more heteroatoms, or is aryl (6-10C), heteroaryl (6-10C), arylalkyl (7-15C) or heteroarylalkyl (7-15C) each of the foregoing either substituted or unsubstituted with one or more substituents selected from the group consisting of halo, -OR', -SR' and -NR'2 where each R' is independently H or alkyl (1-6C) or wherein said aryl or heteroaryl moieties may be substituted with one or more alkyl, alkenyl, or alkynyl, which method comprises contacting a compound of the formula



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wherein R is as defined above

with N-acetyl cysteamine in the presence of a trimethylsilyl triflate catalyst.

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	NheI	SstI
DEBS LOAD AT:	FVEASPHPV <u>LAAALQQT</u> L. DAEGSSAAVV PTLQRGQ.GG MRRFLAAA. . . QAPTEG	Propionyl AT
DEBS AT2:	FIEVSHPHV <u>LASSVQET</u> LD DAE. SDAAVL GTLERDA. GD <u>ADRF</u> LT <u>ALA</u> . . . DAHTRG	
NID AT4:	FVECSHPHV <u>LTVPVQ</u> RT <u>LE</u> DA. GAGAVAV GSLRRDD. GG <u>LRRFLT</u> <u>SA</u> . . . EAQVAG	
FK506 AT9:	FIECSAHPV <u>LL</u> PA <u>L</u> DQE. RT. . . V ASLRTDD. GG <u>WDRFLT</u> <u>LA</u> . . . QAWTQG	Methylmalonyl AT
RAPS AT1:	FVEVSASPV <u>LL</u> Q <u>AM</u> DDDVVT. . . V ATLRRDD. GD <u>ATRMLT</u> <u>LA</u> . . . QAYVEG	
RIF AT1:	FVEVSAHPV <u>TV</u> Q <u>PL</u> SE. . LTGDAI GTLRRD. GG LRR.L. . <u>LA</u> . SMGELFVRG	
DEBS AT6:	FVEMSPHPV <u>LT</u> AAVQ <u>EIAA</u> D. . . . AVAI GSLHRDT. AE. EHLIA <u>ELA</u> . . . RAHTHG. —	
NID AT5:	FLETSHPHM <u>L</u> AAV <u>EQT</u> VT DA. GTDAAVL GTLRRH. GG PRA.LA. . <u>LA</u> . . VCRFAH <u>G</u>	Ethylmalonyl AT
NID LOAD AT:	YLEIGPHPT <u>L</u> T <u>LLHHT</u> LD NP. . TT. . I PTLH <u>RE</u> . PE PETL <u>QIAA</u> . VG. VRTDG	Acetyl AT
NID AT1:	YLEIGAHPT <u>L</u> T <u>LLHHT</u> LD NP. . TT. . I PTLH <u>REH</u> . PE PET <u>TT</u> <u>LA</u> T . . LHTTG	
FK506 AT7:	FLEIGPNQD <u>L</u> SPV <u>VDG</u> I PTQ <u>GTP</u> . EE V <u>QALH</u> <u>TAL</u> . . . RLHTRG	
FK506 AT8:	FVEIGPG <u>QD</u> <u>L</u> SP <u>LV</u> D <u>G</u> I AL <u>ONGT</u> A. DE VEAL <u>HT</u> <u>LA</u> . . . RLFTRG	Malonyl AT
RAPS AT2:	FVEIGADRS <u>L</u> ARL <u>VDG</u> I AMLH <u>GD</u> . . HE AQ <u>AVG</u> <u>AL</u> . . . HLYVNG	
RIF AT2:	FLEIGPG <u>GA</u> <u>L</u> A <u>AMALG</u> <u>TG</u> G <u>PEQ</u> <u>SC</u> . . V ATL <u>RKNG</u> . AE VP <u>DV</u> <u>LT</u> <u>AL</u> . . . ELHVRC	
E. COLI FAS:	Y. EVGPGKV <u>LT</u> GLTKRIV DTL <u>TASAL</u> NE PS <u>AMAA</u> <u>LE</u> L.	

FIGURE 1

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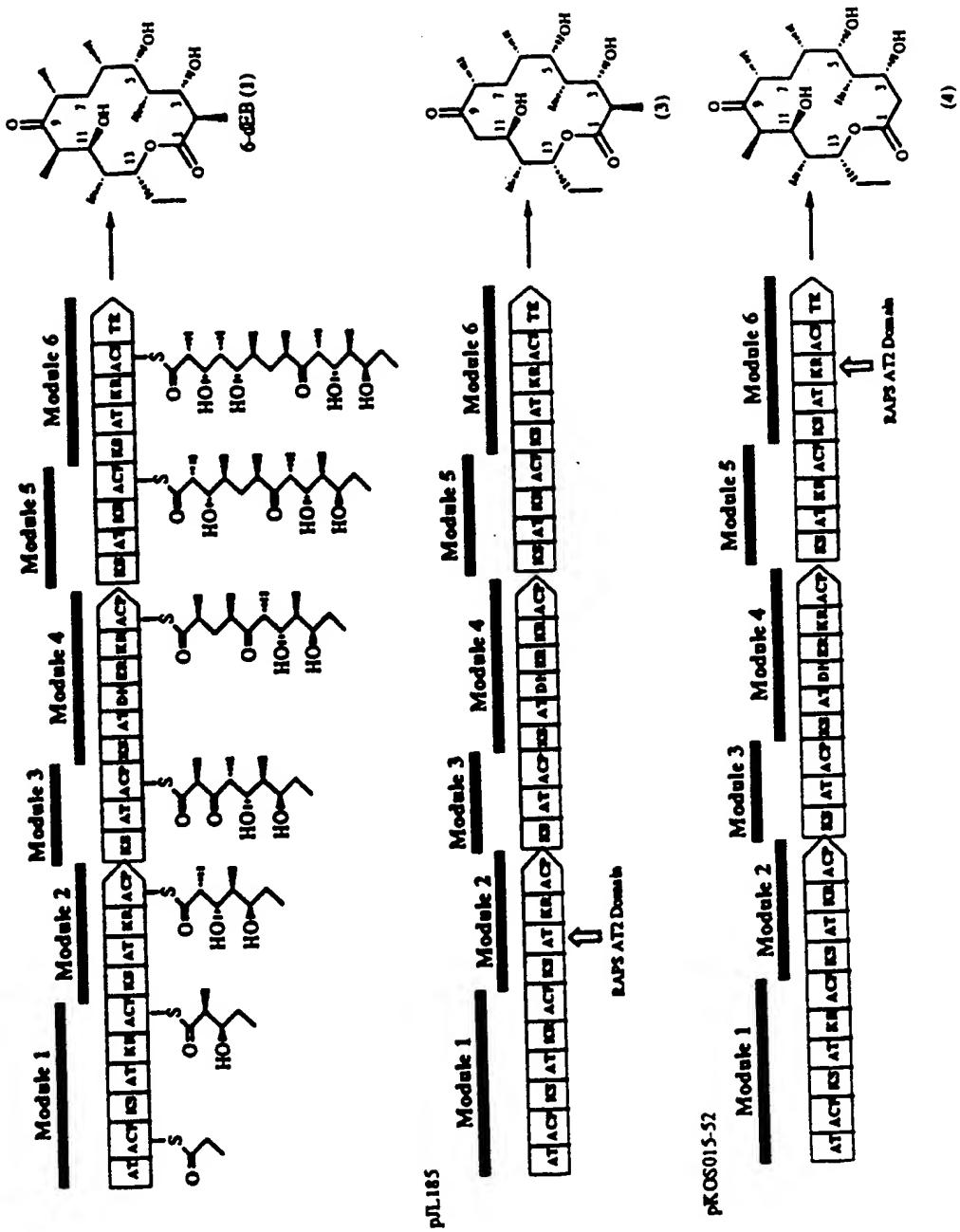


FIGURE 2